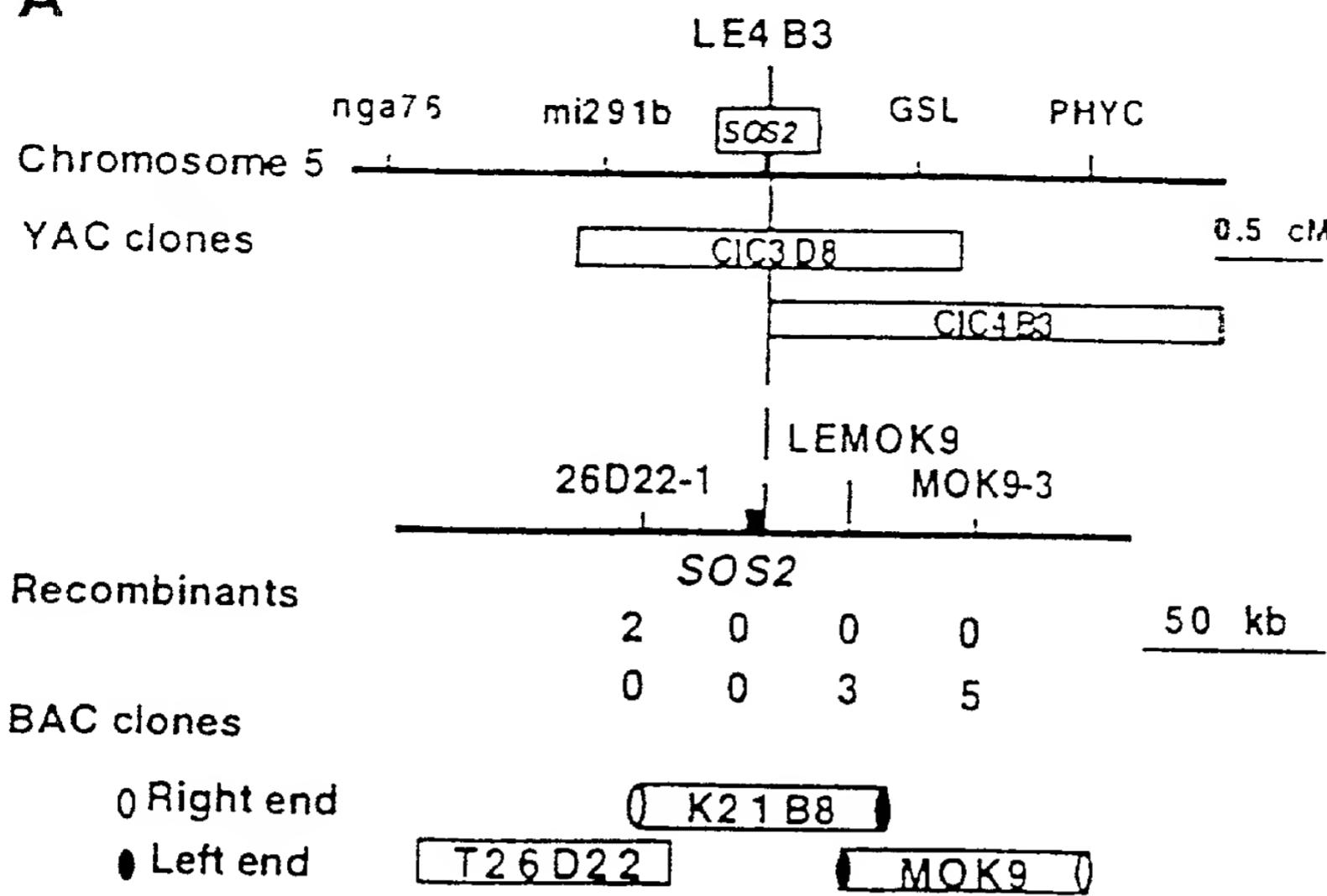


Figure 1

A



B

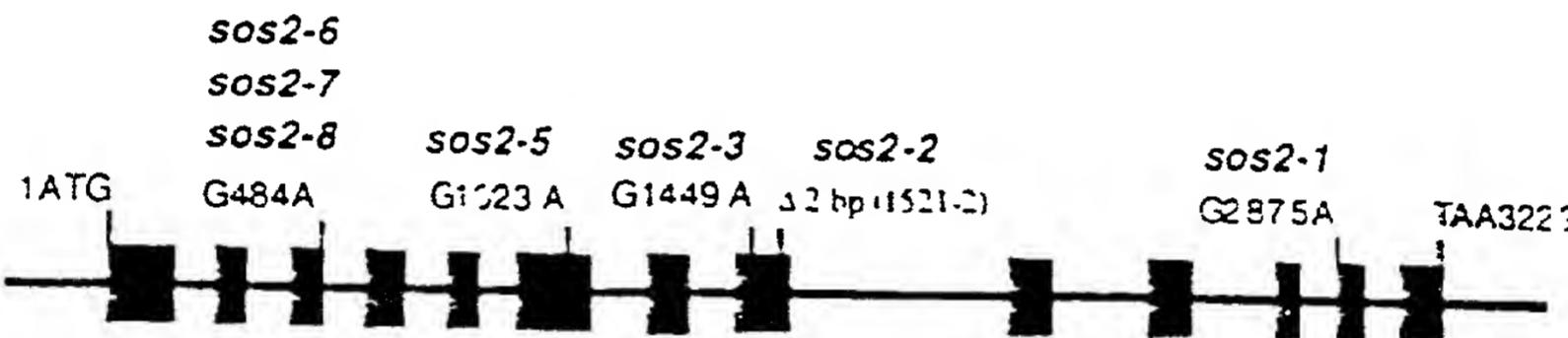


Figure 2

A

Kinase

Regulatory Domain

B

T G A T C A G A T A A A G T T T C T A A G A A T G A C A A A G A A A A T G A G A A G A G T G G G C A A G T A C C A G G T T G T C A C A A T A G G T G A A G G A A C T T T S C T A A G G T T A A G I M T K K M R R V G K Y E V G R T [] E [] T P A K [] K -- I --	Regulatory Domain
--	--------------------------

27 T T G C G A G G A A C A C A G A C T G A T A A T T A S C C A T C A M A T T A T G G T A A G A G T A C A T A C T T A A G A A C A G A A T G
 F A R N T O T G D N V [] I : R A K S T I L K N R M
 -- II --

53 G T G A T C A G A T A A A A G A G A G A T A T C T A T A T G A A G T T T C G T C A C C C G A A C A T A G T S A G G T T O T A T G A G G T T T G
 V D Q I K R [] I S I M X I V R H P N [] V R L Y E V L
 -- III -- -- IV --

79 G C S A G T C C T C G A A A A T A T A T A T A G T T T S G A T T T G T G A C A C G G A G G G T T T G A T A G A A T T T T C A T A A A G G G
 A S P S K I Y I V L E F V T G G E L F D R I V H K G
 -- V --

105 A G G T T C A A G A A G T G A G T C T C G A A A T A C T T C A A C A G C T T S T A G A T G C T T G C T C A T T C A C T G C A A G G G T T T
 R L E E S E S R K Y F G Q I V D [] V A Y [] H C K G V
 -- VI --

131 T A C C A C G T G A C C T A A G C C A G A A A T C T T T A C T C A G A T A C A M A T G G A A A T T G A A G G T T T C G A T T T C G G A C T C A G T
 Y [] R [] K P S [] E L L D T N G N L X Y S [] L S
 -- VII --

157 G C A T T C C T C A G G A A G G A G T A G A A C T T C G T C A C C A C A T T G G A A C T C G G A A C T A T G A G G T C C A G A G G T A C T T A G T
 A C P Q E G V E L I R T T C G [] P X Y V [] V L S
 -- VIII --

183 G G A C A G G G T T A C C A T G G T T C A S C A G C T S A T A T T G G T T C G G G G T T A T T T T C S T A T A T T G C G A T A T T T A
 G Q G Y D G S A A [] I S C [] I L S V I L A G Y L
 -- IX --

209 C C T T T C C G A G A C G G A T C T C C A G G G T T T A C A G A A A A A A T G C A G G A G A G T T T C T T G T C A C C G T G G T T T C C
 P F S E T D L F G L Y R K I N A A E F S C P P W F S
 -- X --

235 G C A G A A G T G A A G T T T T A A T C A T A C A T A C C A T T C A C C C C A A T C C C A A A C A C G T A T T C A A T C A A G G A A T C A A G A A A
 A E V K F L I H R [] L D P N P K T R I Q [] Q G I K K
 -- XI --

261 G A T C T T T G T T C A G A T T A A T T A T G C C T A T A C G G C A A G G G A A G A A G A A G A A C T G A A T T T G G A T A T T C G T C A
 D P W F R L N Y V P I R A R E Z E E V N S D D I R A

287 G T T T T S A T G G A A T T G A G G G C A G T T A T G T A G C G G A G A A T G T A G A G A G A A A T G A T G A A G G G G G C T S A T G A T G A A T G C C
 V F D G I E G S Y V A E N V E R N D E G P L M M N A

313 T T T G A G A T G A T T A C C T T A T C A C A A G G C T T A A T T T A T C G C A C T A T T T G A C A G G G C A C A G G A T T T T T A A A A G G C R A
 F E M I T L S Q G L N L S A L P D R R Q D F V K R Q

339 A C C C G T T T T C T C G A A G G G A A C C T A G T G A G A T T A T G C T A A C T T G A G G C T T S T A G G C A A C T C A A T G G G T T T A A G
 T R F V S R R E P S E I I A N I E A V A N S M G F K

365 T C T C A T A C A C G A A A C T T C A A G A C A A G G C T C G A G G G A T T A T C T C G A T C A A G G G G G A C A S T T A G C T T T G T G A T A G A G
 S H T R N F K T R L E G L S S I K A G Q L A V V I E

391 A T T A C C G A G G T C C C A C C A T C G T T T C A T G G T A G A C G T A A G A A A G G C T G C M G T G A A A C T C T G A A T A T C A C A A G T T C
 I Y E V A P S L F M V D V R K A A G E T L E Y H K F

417 T A C A A G G C T A T T T C G A A A C T C G G A A A C T A T A T G G A G G G C A A C G A A G G A A T A C C A A A G T C A C A G A T T T C C A G A
 Y K K L C S K L E N I I H R A T E G I P K S E I L R

437 A C A A T C A C O T T T G A T C C C A A C T T A A

Figure 3

A

SOS2	1	MTKMRREGRTEVGETLGEETEAKVKEARNTDTCNVAKIEAKSCLLENRMWCG
AMPK	1	MAEHQKHEDGRVHGHYVAGDTLGCTFGKVVKCSHQLTGEKVAKIKIENKOFISLDEVCK
SNF1	43	SLADGAELGNTQIVATLGETSEGRVVKIEYHTTGOKVALKIKIHKVPEPSDCCG
SOS2	36	IKREISIERTKVRHENIPLVIEVESEEKIKAVVBEEMEGGELEFRIVERGRHEESEERPF
AMPK	61	IKREIQNLKLERHPHIIKLYQVISIPTDREBWEYVSEGGELFDYICKGRHEESEARLF
SNF1	101	IEREISYLELDRNPHITKLYDVTKSKDEITVYSEVA-CNELFDYIVCSDKSECEARP
SOS2	116	QQIDVERAHCACGGYHRDLKPEIILLLITNGNEKVSDEGLPAPPOCGVELLRTECGSPN
AMPK	121	QQIDSAVDYCHRAMVHRDLKPEIILLLIPMTEKLADEGLSINTSDC-EFLRTSCGSPT
SNF1	161	QQIDSAVETCHREKUHRDLKPEIILLLTSHBLKIADEGLSINTSDC-NELRTSCGSPT
*		
SOS2	176	VAPEVSGCGIDASADIVSCVILAELEYLPISGTDEGLSRIKINAEFSCPPASA
AMPK	180	VAPEVISCRLYAGHEVDIVSCVILAELEYLPFDEHATLEKKISGVEYHLRSLNR
SNF1	221	VAPEVISCRLYAGHEVTDIVSCVILAELEYLPFDESHVLFKNISGVEYHLRSLNR
SOS2	236	EKFLIHEDDSHEKTRICIOGIRKTBNEN
AMPK	240	SVATLMMNLOEPIKEPLKDIHEHWEKOG
SNF1	280	GAAGLIRRMLIVNPINRISIHEIMODEWEKED

B

SOS2	332	IDEVNHCTRFVSHREPSEIHAMMERVANSVKS---ETRMFKTRLEGESIKASQIAV
YCHK1	369	TOPPERETREESPASRSTIIDLHESLALLHISVTNKYTRIOTIHYANHLSKOLLOCY
HCKK1	371	YRIVHEETRLEPKSYOQKRECEHKGWQ---FSOMNOVTESTERANNKLI
SOS2	399	IEAYEVAPSIVVRAASPTLESCHEREFICSKLEMNIWRATEGZ
YCHK1	440	IELTMCNHLTINHFRNMHPLEPKFFINMVNSIGKPIVLTDVSON
HCKK1	408	YNELEAD-DKILVDPFLSFCGIFERKHELKRIIDIVSSQHWM

Figure 4

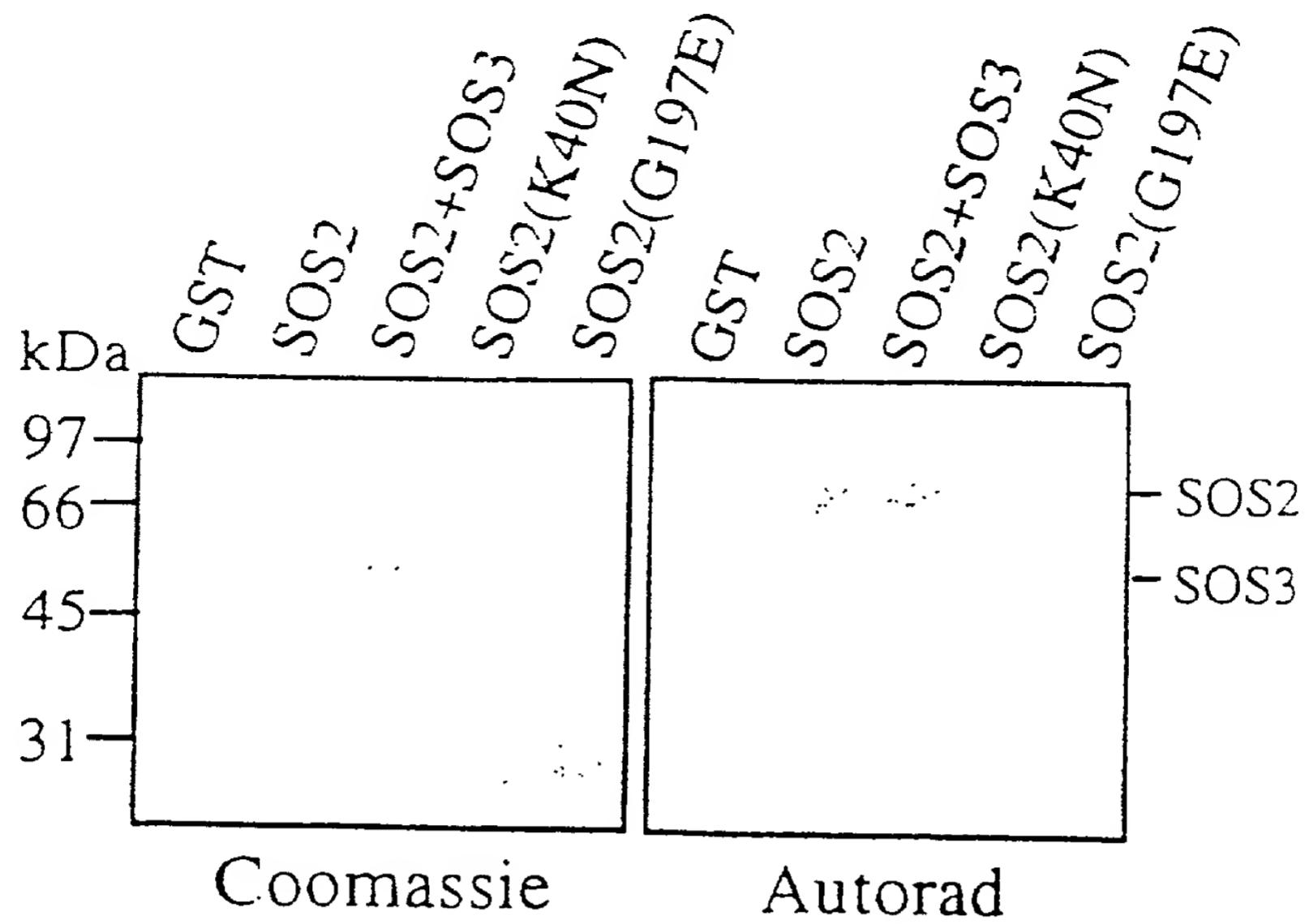


Figure 5

